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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/005,842

DATE: 01/24/2002

TIME: 10:03:46

Input Set : N:\Crf3\RULE60\10005842.raw

Output Set: N:\CRF3\01242002\J005842.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Ni, Jian

6 Gentz, Reiner

7 Yu, Guo-Liang

8 Su, Jeffrey

9 Rosen, Craig A.

11 (ii) TITLE OF INVENTION: Death Domain Containing Receptor 5

13 (iii) NUMBER OF SEQUENCES: 12

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: Human Genome Sciences, Inc.

17 (B) STREET: 9410 Key West Avenue

18 (C) CITY: Rockville

19 (D) STATE: MD

20 (E) COUNTRY: US

21 (F) ZIP: 20850

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk

25 (B) COMPUTER: IBM PC compatible

26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/10/005,842

C--> 31 (B) FILING DATE: 07-Dec-2001

32 (C) CLASSIFICATION:

38 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: 09/042,583

36 (B) FILING DATE:

39 (A) APPLICATION NUMBER: US 60/040,846

40 (B) FILING DATE: 17-MAR-1997

42 (viii) ATTORNEY/AGENT INFORMATION:

43 (A) NAME: Hoover, Kenley

44 (B) REGISTRATION NUMBER: 40,302

45 (C) REFERENCE/DOCKET NUMBER: PF366

47 (ix) TELECOMMUNICATION INFORMATION:

48 (A) TELEPHONE: 3013098504

49 (B) TELEFAX: 3013098439

52 (2) INFORMATION FOR SEQ ID NO: 1:

54 (i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 1600 base pairs

56 (B) TYPE: nucleic acid

57 (C) STRANDEDNESS: single

58 (D) TOPOLOGY: linear

ENTERED

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60      (ii) MOLECULE TYPE: DNA (genomic)
63      (ix) FEATURE:
64          (A) NAME/KEY: sig_peptide
65          (B) LOCATION: 130..283
67      (ix) FEATURE:
68          (A) NAME/KEY: CDS
69          (B) LOCATION: 130..1362
71      (ix) FEATURE:
72          (A) NAME/KEY: mat_peptide
73          (B) LOCATION: 284..1362
76      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
78 CACGCGTCCG CGGGCGCGGC CGGAGAACCC CGCAATCTTT GCGCCCACAA AATACACCGA      60
80 CGATGCCCGA TCTACTTTAA GGGCTGAAAC CCACGGGCCT GAGAGACTAT AAGAGCGTTC      120
82 CCTACCGCC ATG GAA CAA CGG GGA CAG AAC GCC CCG GCC GCT TCG GGG      168
83     Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly
84     -51 -50                      -45                      -40
86 GCC CGG AAA AGG CAC GGC CCA GGA CCC AGG GAG GCG CGG GGA GCC AGG      216
87 Ala Arg Lys Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg
88     -35                      -30                      -25
90 CCT GGG CCC CGG GTC CCC AAG ACC CTT GTG CTC GTT GTC GCC GCG GTC      264
91 Pro Gly Pro Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val
92     -20                      -15                      -10
94 CTG CTG TTG GTC TCA GCT GAG TCT GCT CTG ATC ACC CAA CAA GAC CTA      312
95 Leu Leu Leu Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu
96     -5                      1                      5                      10
98 GCT CCC CAG CAG AGA GCG GCC CCA CAA CAA AAG AGG TCC AGC CCC TCA      360
99 Ala Pro Gln Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser
100     15                      20                      25
102 GAG GGA TTG TGT CCA CCT GGA CAC CAT ATC TCA GAA GAC GGT AGA GAT      408
103 Glu Gly Leu Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp
104     30                      35                      40
106 TGC ATC TCC TGC AAA TAT GGA CAG GAC TAT AGC ACT CAC TGG AAT GAC      456
107 Cys Ile Ser Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp
108     45                      50                      55
110 CTC CTT TTC TGC TTG CGC TGC ACC AGG TGT GAT TCA GGT GAA GTG GAG      504
111 Leu Leu Phe Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu
112     60                      65                      70
114 CTA AGT CCC TGC ACC ACG ACC AGA AAC ACA GTG TGT CAG TGC GAA GAA      552
115 Leu Ser Pro Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu
116     75                      80                      85                      90
118 GGC ACC TTC CGG GAA GAA GAT TCT CCT GAG ATG TGC CGG AAG TGC CGC      600
119 Gly Thr Phe Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg
120     95                      100                      105
122 ACA GGG TGT CCC AGA GGG ATG GTC AAG GTC GGT GAT TGT ACA CCC TGG      648
123 Thr Gly Cys Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp
124     110                      115                      120
126 AGT GAC ATC GAA TGT GTC CAC AAA GAA TCA GGC ATC ATC ATA GGA GTC      696
127 Ser Asp Ile Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val
128     125                      130                      135

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130	ACA	GTT	GCA	GCC	GTA	GTC	TTG	ATT	GTG	GCT	GTG	TTT	GTT	TGC	AAG	TCT	744
131	Thr	Val	Ala	Ala	Val	Val	Leu	Ile	Val	Ala	Val	Phe	Val	Cys	Lys	Ser	
132		140					145					150					
134	TTA	CTG	TGG	AAG	AAA	GTC	CTT	CCT	TAC	CTG	AAA	GGC	ATC	TGC	TCA	GGT	792
135	Leu	Leu	Trp	Lys	Lys	Val	Leu	Pro	Tyr	Leu	Lys	Gly	Ile	Cys	Ser	Gly	
136	155					160					165					170	
138	GGT	GGT	GGG	GAC	CCT	GAG	CGT	GTG	GAC	AGA	AGC	TCA	CAA	CGA	CCT	GGG	840
139	Gly	Gly	Gly	Asp	Pro	Glu	Arg	Val	Asp	Arg	Ser	Ser	Gln	Arg	Pro	Gly	
140					175					180					185		
142	GCT	GAG	GAC	AAT	GTC	CTC	AAT	GAG	ATC	GTG	AGT	ATC	TTG	CAG	CCC	ACC	888
143	Ala	Glu	Asp	Asn	Val	Leu	Asn	Glu	Ile	Val	Ser	Ile	Leu	Gln	Pro	Thr	
144				190				195					200				
146	CAG	GTC	CCT	GAG	CAG	GAA	ATG	GAA	GTC	CAG	GAG	CCA	GCA	GAG	CCA	ACA	936
147	Gln	Val	Pro	Glu	Gln	Glu	Met	Glu	Val	Gln	Glu	Pro	Ala	Glu	Pro	Thr	
148			205				210					215					
150	GGT	GTC	AAC	ATG	TTG	TCC	CCC	GGG	GAG	TCA	GAG	CAT	CTG	CTG	GAA	CCG	984
151	Gly	Val	Asn	Met	Leu	Ser	Pro	Gly	Glu	Ser	Glu	His	Leu	Leu	Glu	Pro	
152		220					225					230					
154	GCA	GAA	GCT	GAA	AGG	TCT	CAG	AGG	AGG	AGG	CTG	CTG	GTT	CCA	GCA	AAT	1032
155	Ala	Glu	Ala	Glu	Arg	Ser	Gln	Arg	Arg	Arg	Leu	Leu	Val	Pro	Ala	Asn	
156	235					240					245				250		
158	GAA	GGT	GAT	CCC	ACT	GAG	ACT	CTG	AGA	CAG	TGC	TTC	GAT	GAC	TTT	GCA	1080
159	Glu	Gly	Asp	Pro	Thr	Glu	Thr	Leu	Arg	Gln	Cys	Phe	Asp	Asp	Phe	Ala	
160				255				260					265				
162	GAC	TTG	GTG	CCC	TTT	GAC	TCC	TGG	GAG	CCG	CTC	ATG	AGG	AAG	TTG	GGC	1128
163	Asp	Leu	Val	Pro	Phe	Asp	Ser	Trp	Glu	Pro	Leu	Met	Arg	Lys	Leu	Gly	
164			270					275					280				
166	CTC	ATG	GAC	AAT	GAG	ATA	AAG	GTG	GCT	AAA	GCT	GAG	GCA	GCG	GGC	CAC	1176
167	Leu	Met	Asp	Asn	Glu	Ile	Lys	Val	Ala	Lys	Ala	Glu	Ala	Ala	Gly	His	
168			285				290					295					
170	AGG	GAC	ACC	TTG	TAC	ACG	ATG	CTG	ATA	AAG	TGG	GTC	AAC	AAA	ACC	GGG	1224
171	Arg	Asp	Thr	Leu	Tyr	Thr	Met	Leu	Ile	Lys	Trp	Val	Asn	Lys	Thr	Gly	
172		300					305					310					
174	CGA	GAT	GCC	TCT	GTC	CAC	ACC	CTG	CTG	GAT	GCC	TTG	GAG	ACG	CTG	GGA	1272
175	Arg	Asp	Ala	Ser	Val	His	Thr	Leu	Leu	Asp	Ala	Leu	Glu	Thr	Leu	Gly	
176	315					320					325				330		
178	GAG	AGA	CTT	GCC	AAG	CAG	AAG	ATT	GAG	GAC	CAC	TTG	TTG	AGC	TCT	GGA	1320
179	Glu	Arg	Leu	Ala	Lys	Gln	Lys	Ile	Glu	Asp	His	Leu	Leu	Ser	Ser	Gly	
180				335				340				345					
182	AAG	TTC	ATG	TAT	CTA	GAA	GGT	AAT	GCA	GAC	TCT	GCC	ATG	TCC			1362
183	Lys	Phe	Met	Tyr	Leu	Glu	Gly	Asn	Ala	Asp	Ser	Ala	Met	Ser			
184			350					355				360					
186	TAAGTGTGAT	TCTCTTCAGG	AAGTGAGACC	TTCCCTGGTT	TACCTTTTTT	CTGGAAAAAG											1422
188	CCCAACTGGA	CTCCAGTCAG	TAGGAAAGTG	CCACAATTGT	CACATGACCG	GTACTGGAAG											1482
190	AAACTCTCCC	ATCCAACATC	ACCCAGTGGA	TGGAACATCC	TGTAACTTTT	CACTGCACTT											1542
192	GGCATTATTT	TTATAAGCTG	AATGTGATAA	TAAGGACACT	ATGGAAAAAA	AAAAAAA											1600
195	(2)	INFORMATION FOR SEQ ID NO: 2:															
197	(i)	SEQUENCE CHARACTERISTICS:															
198	(A)	LENGTH: 411 amino acids															

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199          (B) TYPE: amino acid
200          (D) TOPOLOGY: linear
202          (ii) MOLECULE TYPE: protein
204          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
206 Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys
207 -51 -50          -45          -40
209 Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Pro
210 -35          -30          -25          -20
212 Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
213          -15          -10          -5
215 Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
216          1          5          10
218 Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
219          15          20          25
221 Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
222 30          35          40          45
224 Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe
225          50          55          60
227 Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
228          65          70          75
230 Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe
231          80          85          90
233 Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys
234          95          100          105
236 Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile
237 110          115          120          125
239 Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala
240          130          135          140
242 Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp
243          145          150          155
245 Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly
246          160          165          170
248 Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp
249          175          180          185
251 Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro
252 190          195          200          205
254 Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn
255          210          215          220
257 Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala
258          225          230          235
260 Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp
261          240          245          250
263 Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val
264          255          260          265
266 Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp
267 270          275          280          285
269 Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr
270          290          295          300
272 Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala

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273          305          310          315
275 Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu
276          320          325          330
278 Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met
279          335          340          345
281 Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser
282 350          355          360
284 (2) INFORMATION FOR SEQ ID NO: 3:
286     (i) SEQUENCE CHARACTERISTICS:
287         (A) LENGTH: 455 amino acids
288         (B) TYPE: amino acid
289         (C) STRANDEDNESS: single
290         (D) TOPOLOGY: linear
292     (ii) MOLECULE TYPE: protein
297     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
299 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
300 1          5          10          15
302 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
303          20          25          30
305 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
306          35          40          45
308 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
309          50          55          60
311 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
312          65          70          75          80
314 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
315          85          90          95
317 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
318          100          105          110
320 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
321          115          120          125
323 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
324          130          135          140
326 Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
327          145          150          155          160
329 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
330          165          170          175
332 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
333          180          185          190
335 Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
336          195          200          205
338 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
339          210          215          220
341 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
342          225          230          235          240
344 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
345          245          250          255
347 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
348          260          265          270

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/005,842

DATE: 01/24/2002

TIME: 10:03:48

Input Set : N:\Crf3\RULE60\10005842.raw

Output Set: N:\CRF3\01242002\J005842.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]